

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 3, 2002, 02:14:49 : Search time 1766.36 Seconds  
(without alignments)  
168.104 Million cell updates/sec

Title: US-09-802-359B-1

Perfect score: 1 tgcactgtgaacgttcgagatcga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_estba:\*  
3: em\_estba:\*  
4: em\_estba:\*  
5: em\_estba:\*  
6: em\_estba:\*  
7: em\_estba:\*  
8: em\_estba:\*  
9: em\_estba:\*  
10: em\_estba:\*  
11: em\_estba:\*  
12: em\_estba:\*  
13: em\_estba:\*  
14: em\_estba:\*  
15: em\_estba:\*  
16: em\_estba:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	18.4	83.6	571	10	BM042508 603615795
2	17.8	80.9	561	12	AZ755668 ev02909.x
3	17.4	80.9	961	10	BF971856 602240444
4	17.4	79.1	489	12	AZ060178 RPTC-23-4
5	17.4	79.1	530	12	AZ886419 RPTC-23-1
6	17.2	78.2	374	12	AQ245026 HS-2056_B
7	17.2	78.2	408	12	AZ536502 110300_96
8	17.2	78.2	424	10	BE723539
9	17.2	78.2	463	9	AU083559 AU083559
10	17.2	78.2	479	9	AU089685 AU089685
11	17.2	78.2	513	10	BU094274 BU094274
12	17.2	78.2	519	10	BI796581 H049F08 E
13	17.2	78.2	571	10	BM037907 S114C07 S
14	17.2	78.2	972	12	CNS050PD9 AL347814 Tetradon
15	16.8	76.4	105	9	AA094019 c11619.se
16	16.8	76.4	523	12	AZ483488 1M0309M12
17	16.8	76.4	526	12	AZ501799 1M0340J17

C	18	16.8	76.4	681	9	AV732648
C	19	16.8	76.4	705	9	AM916461
C	20	16.8	76.4	864	12	BH207673
C	21	16.4	74.5	400	9	AM398307
C	22	16.4	74.5	496	9	AM034934
C	23	16.4	74.5	546	12	AZ058706
C	24	16.4	74.5	554	12	AZ280611
C	25	16.4	74.5	599	12	AZ068022
C	26	16.4	74.5	600	12	AZ976014
C	27	16.4	74.5	633	10	BG570577
C	28	16.4	74.5	747	10	BG127461
C	29	16.4	74.5	934	12	CNS027SC
C	30	16.2	73.6	202	9	AA236074
C	31	16.2	73.6	236	9	BI183285
C	32	16.2	73.6	236	10	BP932252
C	33	16.2	73.6	251	9	BB565758
C	34	16.2	73.6	286	9	A1099019
C	35	16.2	73.6	297	9	AA445764
C	36	16.2	73.6	300	10	C11370
C	37	16.2	73.6	307	12	AO581066
C	38	16.2	73.6	317	9	BE119339
C	39	16.2	73.6	360	9	AV189436
C	40	16.2	73.6	398	10	BE428418
C	41	16.2	73.6	401	10	BE275964
C	42	16.2	73.6	416	12	AO646593
C	43	16.2	73.6	432	10	BG813145
C	44	16.2	73.6	434	10	BB851024
C	45	16.2	73.6	434	12	BH187088

#### ALIGNMENTS

RESULT 1  
LOCUS BM042508 571 bp mRNA linear EST 07-NOV-2001  
DEFINITION 603615795F1 NIH\_MGC\_112 Homo sapiens CDNA clone IMAGE:5420734 3',  
RNA sequence.  
ACCESSION BM042508  
VERSION BM042508.1 GI:16771788  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 571)  
NIH-MGC <http://mgc.ncl.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: DCTD/DPF  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1CM1875 row: m column: 23  
High quality sequence start: 44  
High quality sequence stop: 411.  
Location/Qualifiers  
1..571  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5420734"  
/clone\_lib="NIH\_MGC\_112"  
/tissue="Ctpe="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; CDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC library."

BASE COUNT 175 a 120 c 139 g 137 t

Query Match 83.6% Score 18.4; DB 10; Length 571;  
Best Local Similarity 95.0%; Pred. No. 1.5e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tgactgtgaacgttcgagatg 20  
|||||  
DB 504 TGACTGTGAACGTTCTGAGAT 523

RESULT 2  
A2755668/c 561 bp DNA linear GSS 01-MAR-2001  
LOCUS  
DEFINITION ev02909.x1 PAX3 CASTing Library 'ev' Homo sapiens genomic clone  
ACCESSION ev02909 random, DNA sequence.  
A2755668  
VERSION A2755668.1 GI:13175090  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 561)  
AUTHORS Barber,T.D., Barber,M.C., Tomescu,O., Barr,F., Ruben,S. and  
Friedman,T.B.

TITLE Cyclic amplification and selection of target genes regulated by  
Pax3 and PAX3/FKHR in embryogenesis and alveolar rhabdomyosarcoma  
JOURNAL Unpublished (2000)  
COMMENT Laboratory of Molecular Genetics  
National Institute on Deafness and Other Communication Disorders,  
National Institutes of Health  
5 Research Court, Room 2A-15, Rockville, MD 20850, USA  
Tel: 301 402 7580  
Fax: 301 496 7882  
Email: friedman@nidcd.nih.gov  
Plate: 02 row: 9 column: 09  
Seq primer: 21M13 forward primer (ABI)  
Class: random plasmid subclone.  
Location/Qualifiers

FEATURES  
source  
1..561  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="PAX3 CASTing Library 'ev'"  
/sex="Male"  
/lab\_host="DH10B"  
/note="Vector: pGEM-T Easy; Human genomic DNA was  
partially digested with Sau3AI, ligated to ds linkers,  
whole genome PCR-based strategy. DNA fragments containing  
putative PAX3Q+ binding sites were amplified by PCR and  
cloned into pGEM-T Easy (Promega). The ligation products  
were transformed into DH10B electrocompetent cells (Life  
Technologies)."

BASE COUNT 126 a 149 c 152 g 134 t

Query Match 80.9% Score 17.8; DB 12; Length 561;  
Best Local Similarity 90.5%; Pred. No. 2.9e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tgactgtgaacgttcgagatg 21  
|||||  
DB 461 TGACTGTGAACGTCAGAGATG 441

RESULT 3  
BF971856 961 bp mRNA linear EST 22-JAN-2001  
LOCUS  
DEFINITION 602240444F1 NIH-MGC\_46 Homo sapiens cDNA clone IMAGE:4328890 5',  
mRNA sequence.  
BF971856  
ACCESSION BF971856.1 GI:12339071  
VERSION  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 961)  
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.  
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)  
UNPUBLISHED (1999)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM1189 row: h column: 11  
High quality sequence stop: 555.  
Location/Qualifiers

FEATURES  
source  
1..961  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4328890"  
/clone\_lib="NIH-MGC\_46"  
/tissue\_type="leiomyosarcoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: uterus; Vector: pOT87; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the Laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH-MGC  
Library."

BASE COUNT 205 a 225 c 240 g 291 t

Query Match 80.9% Score 17.8; DB 10; Length 961;  
Best Local Similarity 90.5%; Pred. No. 3.4e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gactgtgaacgttcgagatga 22  
|||||  
DB 650 GACTGTGAACGTTCCGATGA 670

RESULT 4  
A2060178 489 bp DNA linear GSS 30-MAR-2000  
LOCUS  
DEFINITION RPCI-23-405E23.TV RPCI-23 Mus musculus genomic clone RPCI-23-405E23  
, DNA sequence.  
A2060178  
ACCESSION A2060178.1 GI:7351427  
VERSION  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurgnathi; Muridae; Murinae; Mus.  
1 (bases 1 to 489)  
AUTHORS Zhao,S., Nierman,W., Feldblum,T., Malek,J., Shatsman,S., Akiret

TITLE  
JOURNAL  
COMMENT

B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.  
Mouse BAC End Sequences from Library RPCI-23  
Unpublished (1999)  
Other GSSs: RPCI-23-405E23.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pje@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics ([inforesgen.com](http://inforesgen.com)). BAC end page: [http://www.tigr.org/tldb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html)  
Plate: 405 row: E column: 23  
Seq primer: SP6  
Class: BAC ends.

FEATURES  
source

Location/Qualifiers  
1. .483  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="RPCI-23-405E23"  
/clone\_1lb="RPCI-23"  
/sex="Female"  
/lab\_host="DH10B"  
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1;  
ECORI; Site\_2: EcorI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcorI and EcorI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcorI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."  
BASE COUNT 162 a 61 c 67 g 198 t 1 others  
ORIGIN

Query Match 79.1%; Score 17.4; DB 12; Length 489;  
Best Local Similarity 94.7%; Pred. NO. 4.2e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 1 tgaactggaacgttcgaga 19  
|||||  
Db 170 TGACTGTGACATTCGACA 152

RESULT 5  
A2886419/c 530 bp DNA linear GSS 05-MAR-2001  
LOCUS  
DEFINITION  
DNA sequence.  
A2886419  
A2886419.1 GI:13205364  
GSS.  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
house mouse.  
Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 530)  
Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.  
Mouse BAC End Sequences from Library RPCI-23  
Unpublished (1999)  
Other GSSs: RPCI-23-18216.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA

FEATURES  
source

Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pje@dejong@mail.chu.org). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/orderingframe.htm>). BAC end page: [http://www.tigr.org/tldb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html)  
Plate: 182 row: I column: 6  
Seq primer: SP6  
Class: BAC ends.

Location/Qualifiers  
1. .530  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="RPCI-23-18216"  
/clone\_1lb="RPCI-23"  
/sex="Female"  
/lab\_host="DH10B"  
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1;  
ECORI; Site\_2: EcorI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcorI and EcorI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcorI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."  
BASE COUNT 174 a 65 c 73 g 218 t  
ORIGIN

Query Match 79.1%; Score 17.4; DB 12; Length 530;  
Best Local Similarity 94.7%; Pred. NO. 4.3e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 1 tgaactggaacgttcgaga 19  
|||||  
Db 189 TGACTGTGACATTCGACA 171

RESULT 6  
AQ245026 374 bp DNA linear GSS 03-OCT-1998  
LOCUS  
DEFINITION  
HS\_2056\_B1\_E03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=5 Row=C, DNA sequence.  
AQ245026  
AQ245026.1 GI:3691600  
GSS.  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS  
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.  
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
99380589

TITLE  
JOURNAL  
COMMENT

Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Sequence Tagged Connector  
Plate: 2056 row: J column: 5  
Class: BAC ends  
High quality sequence stop: 374.  
Location/Qualifiers  
1. .374

BEST AVAILABLE COPY

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Plate=2056 Col=5 Row=J"
/sex="male"
/Note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT      91 a      73 c      92 g      117 t      1 others
ORIGIN

Query Match      78.2%; Score 17.2; DB 12; Length 374;
Best Local Similarity 86.4%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 tgactgtgaacgttcgagatga 22
|||||
Db 207 TGACTGTGACGATGAGATGA 228

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RESULT 7
LOCUS      A2536502      408 bp      DNA      linear      GSS 03-NOV-2000
DEFINITION 110300.96 Planococcus lillacinus DNA Planococcus lillacinus genomic,
ACCESSION  A2536502
VERSION     A2536502.1 GI:11093449
KEYWORDS   GSS.
SOURCE     lllac mealybug.
ORGANISM   Planococcus lillacinus
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
            Aphidiformes; Coccoidea; Pseudococcidae; Planococcus.
            1 (bases 1 to 408)
            Mohan, K.N. and Chandra, H.S.
            Mealybug shotgun sequencing
            Unpublished (2000)
            Contact: Mohan KN
            Microbiology and Cell Biology
            Indian Institute of Science
            Sir C.V. Raman Avenue, Bangalore, Karnataka 560012, India
            Email: mohan@cbl.iisc.ernet.in
            Class: shotgun.
FEATURES
    source      1..408
                /organism="Planococcus lillacinus"
                /db_xref="taxon:40930"
                /clone_lib="Planococcus lillacinus DNA"
BASE COUNT      134 a      83 c      80 g      111 t
ORIGIN

```

```

Query Match      78.2%; Score 17.2; DB 12; Length 408;
Best Local Similarity 86.4%; Pred. No. 4.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 tgactgtgaacgttcgagatga 22
|||||
Db 251 TGACTGTGACGATGATGA 272

RESULT 8
LOCUS      BE723539      424 bp      mRNA      linear      EST 25-APR-2001
DEFINITION 193384 MRC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BE723539
VERSION     BE723539.1 GI:10124826
KEYWORDS   EST.
SOURCE     cow.
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.

```

```

REFERENCE      1 (bases 1 to 424)
AUTHORS      Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Cassa,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Perle,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keeler,J.W.
            Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
            Genome Res. 11 (4), 626-630 (2001)
            21180013
COMMENT      Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single-pass sequencing. Bases called and alt-trimmed with phred
            v0.980904.e. Vector identified by cross-match with the -minscore 18
            and -mismatch 12 options.
            PCR Primers
            FORWARD: AGGAACAGCTATGACCAT
            BACKWARD: GTTTCACGACGACGACG
            Plate: 92 row: E column: 14
            Seq primer: ATTAGTGACATATAG.
FEATURES
    source      1..424
                /organism="Bos taurus"
                /db_xref="taxon:9913"
                /clone_lib="MRC 4BOV"
                /tissue_type="pooled"
                /lab_host="DH10B"
                /note="Vector: pCMV SPORT6; Site:1: XbaI; Site:2: XhoI;
                Library made from pooled tissue from day 20 and day 40
                embryos."
BASE COUNT      107 a      107 c      87 g      123 t
ORIGIN

```

```

Query Match      78.2%; Score 17.2; DB 10; Length 424;
Best Local Similarity 86.4%; Pred. No. 5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 tgactgtgaacgttcgagatga 22
|||||
Db 268 TGACTGTGACGCTGAGATGA 289

RESULT 9
LOCUS      AU083559      463 bp      mRNA      linear      EST 21-MAR-2000
DEFINITION AU083559 Rice green shoot Oryza sativa cDNA clone S14862, mRNA
sequence.
ACCESSION  AU083559
VERSION     AU083559.1 GI:7274015
KEYWORDS   EST.
SOURCE     Oryza sativa.
ORGANISM   Oryza sativa.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 463)
            Sasaki,T. and Yamamoto,K.
            Rice cDNA from green shoot (2000)
            Unpublished (2000)
            Contact: Takuji Sasaki
            National Institute of Agrobiological Resources
            Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
            305-8602, Japan
            Tel: 81-298-38-7441
            Fax: 81-298-38-7468
            Email: tsasaki@abrr.affrc.go.jp, URL:http://rpg.dna.affrc.go.jp/
            PROJECT="Rgp".
            S14862_62.

```

FEATURES	source	location/Qualifiers
		1. 463
		/organism="Oryza sativa"
		/strain="Nipponbare"
		/db_xref="taxon:4530"
		/clone="S14862"
		/clone_1lb="Rice green shoot"
		/note="Green shoot (8 days old)"
BASE COUNT	151 a	74 c 109 g 127 t 2 others
ORIGIN		
Query Match	78.2%	Score 17.2; DB 9; Length 463;
Best Local Similarity	86.4%	Pred. No. 5.1e+02;
Matches 19; Conservative	0; Mismatches 3; Indels 0; Gaps 0;	
OY	1 tgactgtgaacgttcagatga 22	
DB	151 TCAGTGTGAATGTTAGACATGA 172	

RESULT	10			
LOCUS	AU089685			
DEFINITION	AU089685 Rice callus <i>Oryza sativa</i> cDNA clone C40060, mRNA sequence.	479 bp	mRNA	linear EST 27-APR-2000
ACCESSION	AU089685			
VERSION	AU089685.1	GI:7652165		
KEYWORDS	EST.			
SOURCE	<i>Oryza sativa</i> .			
ORGANISM	<i>Oryza sativa</i>			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; <i>Oryza</i> .			
AUTHORS	1 (bases 1 to 479)			
TITLE	Sasaki, T. and Yamamoto, K.			
JOURNAL	Rice cDNA from callus (2000)			
COMMENT	Unpublished (2000)			
	Contact: Takuji Sasaki			
	National Institute of Agrobiological Resources			
	Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki			
	305-8602, Japan			
	Tel: 81-298-38-7441			
	Fax: 81-298-38-7468			
	Email: tssasaki@affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/			
	PROJECT = RGP.			
	C40060_32.			

FEATURES		source		Location/Qualifiers	
		1.	479		
		/organism="Oryza sativa"			
		/strain="cultivar Nipponbare, sub-species Japonica"			
		/db_xref="taxon:4530"			
		/clone="C40060"			
		/clone_id="Rice callus"			
		/note="vector: pbluescript II SK+ site_1: SalI; site_2: NotI; cDNA prepared from rice callus mRNAs by using oligo(dt) as a primer and ligating to the SalI-NotI site of pbluescript II SK+ phagemid."			
BASE COUNT	149 a	96 c	104 g	130 t	
ORIGIN					
Query Match		78.2%	Score 17.2;	DB 9;	Length 479;
Best Local Similarity		86.4%;	Pred. No. 5.2e+02;		
Matches 19;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;	
QY	1	ttacgtgtgaacgttcgagatga	22		
DB	299	tgagtgtaattgttagagatga	320		
RESULT	11				
BT094274					
LOCUS	BT094274	513 bp	mRNA	linear	EST 12-DEC-2001

```

DEFINITION      BU094274 NIBB Mochli normalized Xenopus early gastrula library
ACCESSION       BU094274
VERSION          BI094274.1
KEYWORDS         GI:17594227
SOURCE           EST
ORGANISM         African clawed frog.
XENOPUS laevis
SOURCE           Xenopus laevis
REFERENCE        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS          Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
                  Xenopodinae; Xenopus.
                  1 (bases 1 to 513)
                  Kitayama,A., Terasaka,C., Mochli,M., Ueno,N., Shin-I,T. and Kohara
                  Y.
FEATURES         Expressed genes in X. laevis embryo
                  Unpublished (2001)
                  Contact: Tadasu Shin-I
                  Center:For Genetic Resource Information
                  National Institute of Genetics
                  111 Yata, Mishima, Shizuoka 411-8540, Japan
                  Tel: 81-559-81-6856
                  Fax: 81-559-81-6855
                  Email: tshin@genes.nig.ac.jp.
                  Location/Qualifiers
                    1..513
                    /organism="Xenopus laevis"
                    /db_xref="taxon:8355"
                    /clone="XU144p18"
                    /clone_1db="NIBB Mochli normalized Xenopus early gastrula
                    library"
                    /tissue_type="whole embryo"
                    /dev_stage="stage 10.5"
                    /dev_stage="stage 10.5"
BASE COUNT      106 a 129 c 153 g 119 t
ORIGIN
Query Match      78.2%; Score 17.2; DB 10; Length 513;
Best Local Similarity 86.4%; Pred. No. 5.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY               1 tgactctgaacgttcagatga 22
                  ||||| ||||| ||||| |||||
DB               198 ttccctgagacacttgcgatga 219
RESULT 12
BI796581         519 bp. mRNA linear EST 02-OCT-2001
LOCUS            H049F08 EndospERM library from Oryza sativa (10 days after anthesis
DEFINITION       ) Oryza sativa cDNA clone H049F08, mRNA sequence.
ACCESSION        BI796581
VERSION          BI796581.1
KEYWORDS         GI:15848305
SOURCE           EST.
ORGANISM         Oryza sativa.
Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 519)
Dong,H.T., Li,D.B., Zhang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
A Gene Expression Screen in Oryza sativa
Unpublished (2001)
Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaxuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.
Location/Qualifiers
                  1..519
                  /organism="Oryza sativa"
FEATURES
SOURCE

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/db_xref="taxon:4530"
/clone_lib="Endosperm library from Oryza sativa (10 days
after anthesis)"
/tissue_type="Endosperm"
/dev_stage="10 days after anthesis"
/Note="Vector: psp0rt2"
BASE COUNT      149 a      98 c      121 g      151 t
ORIGIN

Query Match      78.2% Score 17.2: DB 10: Length 519:
Best Local Similarity 86.4%: Pred. No. 5.4e+02:
Matches 19: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

Oy 1 tgactgtgaacgttcgagatga 22
    ||| ||||| ||| ||||| |||
Db 266 TGAGTGTGAATGTTAGAGATGA 287

RESULT 13
BM037907      571 bp mRNA linear EST 06-NOV-2001
LOCUS      S114c07 Stem library from Oryza sativa (3-5 leaf stage) Oryza
DEFINITION      BM037907
ACCESSION      BM037907
VERSION      BM037907.1 GI:16753528
KEYWORDS      EST.
SOURCE      Oryza sativa.
ORGANISM      Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 571)
AUTHORS      Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
              ,H.F., Jiang,Y.X., Yu,F.C., Gao,O.K. and Lou,Y.C.
              A Gene Expression Screen in Oryza sativa
              Unpublished (2001)
TITLE      Contact: Dong HT
JOURNAL      Laboratory of Functional Genetics
COMMENT      Bio-technology Institute of Zhejiang University
              Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
              Tel: 0086-571-86892051
              Fax: 0086-571-86961525
              Email: htdong@zjuem.zju.edu.cn
              Seg primer: M13 forward primer.
              Location/Qualifiers
                1..571
                /organism="Oryza sativa"
                /db_xref="taxon:4530"
                /clone_lib="S114c07"
                /clone_1id="Stem library from Oryza sativa (3-5 leaf stage
                )"
                /tissue_type="Stem"
                /dev_stage="3-5 leaf stage"
                /note="Vector: psp0rt2"
BASE COUNT      158 a      101 c      133 g      177 t
ORIGIN

Query Match      78.2% Score 17.2: DB 10: Length 571:
Best Local Similarity 86.4%: Pred. No. 5.5e+02:
Matches 19: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

Oy 1 tgactgtgaacgttcgagatga 22
    ||| ||||| ||| ||||| |||
Db 179 TGAGTGTGAATGTTAGAGATGA 200

RESULT 14
CNS05PD9      972 bp DNA linear GSS 26-MAY-2000
LOCUS      Tetradon nigroviridis genome survey sequence T7 end of clone
DEFINITION
```

```

005F08 of library A from Tetradon nigroviridis, genomic survey
sequence.
AL347814
AL347814.1 GI:8241584
GSS: genome survey sequence.
Tetradon nigroviridis.
Tetradon nigroviridis.
Tetradon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontiformes;
Tetradontidae; Tetradon.
1 (bases 1 to 972)
Roest-Crolius,H., Jalllon,O., Dasilva,C., Fitzames,C., Fisher,C.,
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis
Unpublished
2 (bases 1 to 972)
Roest-Crolius,H., Jalllon,O., Dasilva,C., Bonneau,L., Fisher,C.,
Bernot,A., Fitzames,C., Winkler,P., Brotlier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence
Unpublished
3 (bases 1 to 972)
Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradon.
Location/Qualifiers
  1..972
  /organism="Tetradon nigroviridis"
  /db_xref="taxon:99883"
  /clone_1id="A"
  /note="Genoscope sequence ID : COAA005DC04C1-end : 77"
BASE COUNT      195 a      268 c      199 g      297 t
ORIGIN

Query Match      78.2% Score 17.2: DB 12: Length 972:
Best Local Similarity 86.4%: Pred. No. 6.7e+02:
Matches 19: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

Oy 1 tgactgtgaacgttcgagatga 22
    ||| ||||| ||| ||||| |||
Db 46 TGCGTGTGAAGTTCGAGATGA 25

RESULT 15
AA094019      105 bp mRNA linear EST 25-OCT-1996
LOCUS      c11619.seq.F Human fetal heart, Lambda zap Express Homo sapiens
DEFINITION      AA094019
ACCESSION      AA094019
VERSION      AA094019.1 GI:1639612
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 105)
AUTHORS      Ilew,C.C.
TITLE      CDNAs from fetal heart (1996)
JOURNAL      Unpublished (1996)
COMMENT      Contact: Ilew CC
              Brigham and Women's Hospital
              Harvard Medical School
              75 Francis St. Boston, MA 02115, USA
```

Tel: 6177328915  
Fax: 6179750995

Email: c1iew@rics.bwh.harvard.edu  
PCR Primers

FORWARD: 5' GCCAGCTCGAATTAACCTCCTCAATAAGG 3'  
BACKWARD: 5' CCAGTGAATGTGATACGACCTCCTATAGGCG 3'  
Seq primer: 5' GAAATTACCTCCTCAATAAGG 3'

## FEATURES

source

1.105  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Human fetal heart, Lambda ZAP Express"  
/lab\_host="E. coli XL1-Blue"  
/note="Vector: Lambda ZAP Express; Site\_1: EcoRI; Site\_2:  
XhoI; mRNA was purified from human fetal hearts (8-10  
weeks). cDNA was synthesized using a XhoI-Oligo dT  
adaptor-primer. EcoRI adaptors were ligated, followed by  
digestion with XhoI, for directional cloning into  
predigested Lambda ZAP Express."  
BASE COUNT 31 a 21 c 16 g 37 t  
ORIGIN

Query Match 76.4%; Score 16.8; DB 9; Length 105;  
Best Local Similarity 90.0%; Pred. No. 4.8e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tgactgtgacgttcgagat 20  
|||||  
Db 43 TGAAGTGAACCTCCTCAAT 62

Search completed: September 3, 2002, 03:50:12  
Job time: 5723 sec

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